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Matching the proteome to the genome

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Supplementary Fig. S1

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      *      20      *      40      *      60      *
Cimm-Aat2 : -----MSPPPRPSLSFTPSSSSPSSSSLSLHRHSSKATSSSTALSTAQSRLSTISKHIMASSSSSPS : 62
Pchr-Aat2 : -----MTSTQSARDRLSSLSHHIMGSSS--PS : 25
Aory-Aat2 : -----MSP-----STAS-----SSSTARNRLASLSAQIMGSAS-PS- : 32
Afum-Aat2 : -----MSSPRLPTPTTTTTTTTTTTTTTASTSSSSSFSSSSSSSSSVARNRLASISSQIMGSSS-PS- : 60
Anid-Aat2 : -----MSTP-----SSVSS-----SYSAAKSRLASLASHIMGSSS-ASP : 34
Ncra-Aat2 : MAPASTLLRAAAPAPHAHTSFPSHHTPTSSPNRTTITNTNPSANSTSSTPLHRIQTIAKHMLALPQI---T : 67
Mgri-Aat2 : -----MSAKATRGSTSSSTPQNSSS-----SQSQSQSTAVSYIRNIANHMMASPS---T : 47
Bfuc-Aat2 : -----MSQLSN---T : 7
Sscl-Aat2 : -----MSELSA---T : 7
Pnod-Aat2 : -----MPPPSRQPPSST-----SSSSQTSNLRLSQISTQLAPMAA---T : 36
Ccin-Aat2 : -----MATRLKQLFGHLLSSSDM---T : 18
Scer-Aat2 : -----MS : 2
Cgla-Aat2 : -----MS : 2
Klac-Aat2 : -----MS : 2
Agos-Aat2 : -----MS : 2
Calb-Aat2 : -----M : 1
Dhan-Aat2 : -----M : 1

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      80      *      100      *      120      *      140
Cimm-Aat2 : IFTANVVPKAPEDPLFGIMRAYRADPSDKKVDLIGIGAYRDDNAKPWILPVVRKADEAIRNDPTVNHEYLP : 132
Pchr-Aat2 : VFTAATVAAAPEDPLFGIMKAYREDPSDKKVDLIGIGAYRDNNARPWILPVVKKADDAIHNDPTLNHEYLS : 95
Aory-Aat2 : VFSTSVVPAAPEDPLFGLAQAFRNDPSDKKVDLIGIGAYRDDNAKPWILPVVRKAGDLIRNDPSINHEYLP : 102
Afum-Aat2 : VFSTAVVPAAPEDPLFGLAQAFRQDPSPDKKVDLIGIGAYRDNNAKPWILPVVKKADEAIRNDPNLNHEYLP : 130
Anid-Aat2 : VFSTAVVPSAPEDPLFGLAQAYRQDPSPDKKVDLIGIGAYRDDNAKPWVLPVVKKADELIRNDPNLNHEYLP : 104
Ncra-Aat2 : SFPAEVVPQAPEDPLFGIARAFKADPSQKVDLIGIGAYRDENAKPWVLPVVKKADEIIRNDPEANHEYLP : 137
Mgri-Aat2 : IFTADVVPQAPEDPLFGIMAAAYRADESPDKVDLIGIGAYRDDNAKPWVLPVVKKADEIIRNDPSANHEYLP : 117
Bfuc-Aat2 : SFPEGTVPAAPEDPLFGIMAAAYRADTFDKKVDLIGIGAYRDNNAKPWVLPVVKKADEIIRNDPALNHEYVP : 77
Sscl-Aat2 : SFPENAVPKAPEDPLFGIMAAAYRADTFDKKVDLIGIGAYRTNDAKPWVLPVVKKADEIIRNDPALNHEYLP : 77
Pnod-Aat2 : AFDANVVPQAPEDPLFGIMAAAYRRNDNDPKVDLIGIGAYRDNNAKPWILPVVKKADEIIRNDPDNLNHEYLP : 106
Ccin-Aat2 : AELWQNVPLAPPDSIFKLTAAAYKADTFEKKVNLGVGAYRDDNAKPWVLPVVKKATERLLKDDTLNHEYLP : 88
Scer-Aat2 : ATLFNNIELLPPDALFGIKQRYGQDQRATKVDLIGIGAYRDDNGKPWVLPVSKAAEKLHNDSSYNHEYLG : 72
Cgla-Aat2 : ATIFNNIEELPADALFGIKQRYNQDTRATRVDLIGIGAYRDDQGPWVLPVSRMAERATQEDPSYNHEYLG : 72
Klac-Aat2 : RTILNNIQELPGDALFAIKQRLAEDPRSAKVDLIGIGAYRDEGKPWVLPVAVRKAETLIHSDASFNHEYLG : 72
Agos-Aat2 : LTAFNQLEILPPDALFDVKKRLTQDTRSFKVDLIGIGAYRDENGKPWVLPVREAEKQLMADPGYNHEYLG : 72
Calb-Aat2 : AP-FAGIKELPPDPLFGIKARYNADSRTNKVDLIGIGAYRDNNGKPWILPAVRQAEQKLINSPDYNHEYLS : 70
Dhan-Aat2 : SKYFSSIKELEPPDPLFGIKARYTADDRSDKVDLIGIGAYRDNNGKPWILPAVRKAQEVKLVNSEEYNHEYLS : 71

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      *      160      *      180      *      200      *
Cimm-Aat2 : IAGLPDLAPAAQKLILGADSPAITEKRVTTFQTIISGTGAVHLGGLFLSKFYFAN----PKPATIYLSPTW : 198
Pchr-Aat2 : IGGIAEFTSAAQKLIVGADSPAIREKRICITLQTIISGTGAVHLGGLFLSKFHPQ-----KPAIYLSNPTW : 159
Aory-Aat2 : IKGLPEFTSAAQKVLIGSDSPAIREQRVATFQTIISGTGAVHLGALFLAKEHPAN----PKPTVYLSNPTW : 168
Afum-Aat2 : IKGLPDFTSAAQKLIVGADSPAIREKRVCTLOAIISGTGALHLGALFLAKEHPVP---PK--VYLSPTW : 194
Anid-Aat2 : IKGLAEYTTAAQKLIGADSPAIAENRVCTFQTIISGTGAVHLGALFLAREHEAT---PKPTLYLSPTW : 170
Ncra-Aat2 : IAGLASLTSKAAELVVGASAPAITTEGRVASTIOTISGTGACHLGGLFLSRFYNPYGDASKKPTVYLSNPTW : 207
Mgri-Aat2 : ITGLASFTSKAGELMIGADTPAK--GRVTSVQTIISGTGALHLGALFLQKEYR---KVYSNSVHLNPTW : 182
Bfuc-Aat2 : IAGLNTFTSAAAKLMIGSDSPALAEKRSCSVQTIISGTGAVHLGALFLIKKFYP---GSP--TVYFSNPTW : 141
Sscl-Aat2 : IAGLNTFTSAAAKLMIGADSPALADKRAYSIQAIISGTGAVHLGALFFKKFYP---NSP--TVYLSNPTW : 141
Pnod-Aat2 : IAGLADFTSASQKLVLGGDSPAIKEKRVTSLQTIISGTGAVHLGALFLAKEFYK---KGSQRLAYFSPTW : 172
Ccin-Aat2 : ITGLPEFTSAAAKLILGPDSPAIKENRAVAVQTIISGTGANHLGALFLSRFYGWN---GEPRVYLSNPTW : 154
Scer-Aat2 : ITGLPSLTSNAAKIIFCTQSDAFQEDRVISVQSLSGTGALHISAKFFSKFFPDK-----LVYLSKPTW : 135
Cgla-Aat2 : INGLPSLSSAAANVIFGEDSPALKEGRTISVQSLSGTGALHIAAKFISKEAADK-----KIYLSQPTW : 135
Klac-Aat2 : IAGLPALTSGAQKVLIGDDSSALAEKRVVSAQSLSGTGALHIAAKFIQKELPGK-----LLYVSDPTW : 135
Agos-Aat2 : IAGLEEFRAAAARVLLGEDSEALAEGRVVSQVSIISGTGALHVAAKLLAKTVPDA-----TVYMSDPTW : 135
Calb-Aat2 : ISGFAPFTESAQKVLIGENSLAIKDKKIVSQSLSGTGALHLAGVFIKEFYQGN-----HTIYLSQPTW : 134
Dhan-Aat2 : ISGYQPFLETSAKVLIGNNSAAIKESRVTISQSLSGTGALHLAGAFLEKEFTTES--KKAPT VYLSNPTW : 139

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| | | | | | | | | | |
|-------------|-------|----------|-----------|-------|----------|--------|----------|--------|------------------------------|
| | | 220 | * | 240 | * | 260 | * | 280 | |
| Cimm-Aat2 : | ANHQ | IFTNVNLT | TAYYPY | SAQT | TKGLDID | GMLAAI | TRAAPQGS | IFVLH | CAHNPTGVDPTQDQWKQIAAA : 268 |
| Pchr-Aat2 : | ANHNQ | IFSNVGL | TLAKYPYF | SAKT | TKGLDFNG | MIAALE | APQGSV | ILLH | CAHNPTGVDPTEDQWKQIAEV : 229 |
| Aory-Aat2 : | ANHNQ | IFTNVGL | SLATYPYF | DAKT | TKGLNFD | GMLNGT | IREAPAGS | VILLH | CAHNPTGVDLTQDQWKQIAVV : 238 |
| Afum-Aat2 : | ANHHQ | IFTNVGL | KLANYPYF | SAKT | TKGLDFD | GMLGAL | REAPPGS | IIVLH | CAHNPTGVDLTQDQWKQIAVV : 264 |
| Anid-Aat2 : | ANHHQ | IFTNVGFT | LANYPYF | SPQT | TKGLDFD | GMINAL | RSAAPGS | IILLH | CAHNPTGVDLTQEQWKQIAVV : 240 |
| Ncra-Aat2 : | ANHNQ | IFSNVGL | PIAQYPYF | DQKT | TKGLDID | GMLKAL | SDAPERS | IILLH | CAHNPTGVDPTLAQWKQIAEI : 277 |
| Mgri-Aat2 : | ANHNQ | IFSNVQV | PTTYPYF | DKGT | TKGLDFE | GKATLN | NAEHSI | IILLH | CAHNPTGVDPTQGWREIAEI : 252 |
| Bfuc-Aat2 : | ANHNQ | IFSNVHL | PTATYPYF | SKST | TKGLDFD | GKNTIQ | NAPDKS | IILLH | CAHNPTGVDPTQDQWKQIAVL : 211 |
| Sscl-Aat2 : | VNHQ | IFSNVHL | PVATYPYF | SKST | TKGLDFD | GKSTIQ | NAPDKS | VILLH | CAHNPTGVDPTKDQWKQIAVL : 211 |
| Pnod-Aat2 : | ANHFQ | IFSNVGL | EYKTPYF | SKQT | TKGLDFD | GMISSL | QDAPEG | SIILLH | CAHNPTGVDPTQDQWKQIAEV : 242 |
| Ccin-Aat2 : | ANHHA | IFRNVGI | EPVDYPY | NPQT | TISLDFD | RDLIDS | LKEAPARS | VFLLH | CAHNPTGVDPTPEQWEATADV : 224 |
| Scer-Aat2 : | ANHMA | IFENQGL | KTATYPY | WANET | TKSLDLN | GFLNAI | QKAPEG | SIFVLH | CAHNPTGLDPTSEQWQIVDA : 205 |
| Cgla-Aat2 : | ANHNA | IFKAQGL | ETASYPY | WKSS | TKSLDLE | GFLSAI | ESAPKGS | SIFLLH | CAHNPTGLDPTSEKQWVILDA : 205 |
| Klac-Aat2 : | ANHVS | IFESQGV | KTATYPY | WDAAT | TKSLDLE | GFLKAI | ESSPRGS | VFLLH | CAHNPTGLDPTTEAQWEKILSA : 205 |
| Agos-Aat2 : | GNHF | AVFETQ | GLRTATYPY | WDAAT | RSLDME | GVLGAL | GAAPRG | SVFVLH | CAHNPTGLDPTNEEQWVILDA : 205 |
| Calb-Aat2 : | ANHKQ | IFEYIGF | KVASYPY | WNND | TKSLDLS | GFLKAI | SSAPDG | SVFLLH | CAHNPTGLDPTNQSQWDEILAA : 204 |
| Dhan-Aat2 : | ANHNQ | IFTSLGL | QVEKYPY | WNDT | TKSLNLK | GFLSTI | QEAPKN | SIFVLH | CAHNPTGLDATKEQWEEILEA : 209 |

| | | | | | | | | | | | | | | | |
|-------------|--------|--------|----------|-------|---------|---------|----------|-------|--------|-------|---------|-------|-----------|-----------|-------|
| | | * | 300 | * | 320 | * | 340 | * | | | | | | | |
| Cimm-Aat2 : | MRERN | HFPFFD | TAYQGF | ASGDL | LARDAWS | IRYFVE | QGG--- | FELC | VQAQSF | AKNFG | GLYGER | AGAFH | FVSAPG- | : 334 | |
| Pchr-Aat2 : | MRSRS | HFPFFD | TAYQGF | ASGDL | LVDRD | SWAIRY | FVEQG--- | FELC | VQAQSF | AKNFG | GLYGERT | GAFH | FVSAPG- | : 295 | |
| Aory-Aat2 : | MRERR | HFPFFD | TAYQGF | ASGDL | LNDRD | AWAVRY | FIEQG--- | FELC | VQAQSF | AKNFG | GLYGQRA | GAFH | FVSAPG- | : 304 | |
| Afum-Aat2 : | LRERQ | HFPFFD | TAYQGF | ASGDL | SRD | SWAIRY | FVDOG--- | FELC | VQAQSF | AKNFG | GLYGORT | GAFH | FVSAPG- | : 330 | |
| Anid-Aat2 : | MRDRS | HFPFFD | CAYQGF | ASGDL | LARDAW | AIRYFVE | QGG--- | FELC | VQAQSF | AKNFG | GLYGERT | GAFH | FVSAPG- | : 306 | |
| Ncra-Aat2 : | MAAKG | HFPFFD | TAYQGF | ASGDL | DRD | SAIRL | FVELG--- | FELV | VQAQSF | AKNFG | GLYGQRA | GCFH | FISAPS- | : 343 | |
| Mgri-Aat2 : | MKAKK | HFPFFD | CAYQGF | ASGDL | DRD | AWAVRY | FVEQG--- | FELV | VQAQSF | AKNFG | GLYGER | AGCFH | VVSAPA- | : 318 | |
| Bfuc-Aat2 : | LKQKQ | HFPFFD | CAYQGF | ASGDL | LAKDAW | AVRYFIE | QGG--- | FELC | VQAQSF | AKNFG | GLYSERT | GCFH | FTGAG- | : 277 | |
| Sscl-Aat2 : | LKQKQ | HFPFFD | CAYQGF | ASGDL | LANDAW | AIRYFIE | QGG--- | FELC | VQAQSF | AKNFG | GLYSER | AGCFH | FTGAA- | : 277 | |
| Pnod-Aat2 : | IRSKK | HFPFFD | TAYQGF | ASGDL | LARDG | WAIRYF | IEQG--- | FELC | VQAQSF | AKNFG | GLYGER | AGCFH | FTISPS- | : 308 | |
| Ccin-Aat2 : | MLERGH | YAFD | CAYQGF | ASGDL | DKDAW | VRREFE | KN--- | VPLL | VCSQ | FAKN | AGLYG | ERVGA | LHVVS---- | : 287 | |
| Scer-Aat2 : | TASKN | HIALFD | TAYQGF | ATGDL | DKDAY | AVRLG | VEKLST | VSPV | FVCQ | SFAKN | AGMYG | ERVGC | FHLALTKQ- | : 274 | |
| Cgla-Aat2 : | LVKGD | HIALFD | SAYQGF | ASGDL | DKDAF | AVRLG | VEKLAST | SPIF | VVCQ | SFAKN | VGMYG | ERVGC | FHLTLPKQ- | : 274 | |
| Klac-Aat2 : | CVKND | IIPL | FDSAYQGF | ASGSL | TND | FAVRLG | VKKFAE | SAPIF | ICQ | SFAKN | VGMYG | ERCGC | IHILVPRQE | : 275 | |
| Agos-Aat2 : | VAARE | HTVL | FDSAYQGF | ASGSL | LARDAY | ALRAGL | RRLA | EVTP | VLV | CQ | SFAKN | IGMYG | ERVGA | LHVLP | : 274 |
| Calb-Aat2 : | LEKKK | HFIIF | DSAYQGF | ASGDL | LEKDAY | PIRKAI | DSKVIT | SPII | ICQ | SFAKN | VGMYG | ERVGA | IHVLPST-- | : 272 | |
| Dhan-Aat2 : | LAKNE | HLAL | YDSAYQGF | ASGNL | DNDG | FAVRLA | WDSKKL | KTP | IVIC | Q | SFAKN | CGMYG | ERVGA | IHVLP---- | : 275 |

| | | | | | | | | | | | | | | | | | | | |
|-------------|-------|-------|---------|-------|-------|-------|-------|--------|-------|-------|--------|--------|-------|-------|----------------|----------------|----------------|------------------|--------------|
| | | 360 | * | 380 | * | 400 | * | 420 | | | | | | | | | | | |
| Cimm-Aat2 : | --PHA | ADSTA | HLIASQ | LAIL | LORSE | ISNPP | PAYG | ARIAS | LIILN | SEELF | AEWEAD | DLRT | MSGR | IMEM | RKGLRERL : 402 | | | | |
| Pchr-Aat2 : | --PDA | APACS | NIASQ | LAIL | LORSE | ISNPP | PAYG | ARIAS | RVLND | PVLF | KEWEAD | DLRT | MSGR | ILEMR | QGLRDL : 363 | | | | |
| Aory-Aat2 : | --ATA | KNDIA | NVASQ | LAIL | LORSE | ISNPP | PAYG | ARIAS | RI | LNDA | TFLFA | EWED | DLRT | MSGR | IAEM | RKGLRERL : 372 | | | |
| Afum-Aat2 : | --PDA | STAN | ANIASQ | LAIL | LORSE | ISNPP | PAYG | ARIAS | RI | LN | DPQ | LFA | EWED | DLRT | MSGR | IAEM | RKGLRERL : 398 | | |
| Anid-Aat2 : | --PEA | AQSS | AHVASQ | LAIL | LORSE | ISNPP | PAYG | ARIAS | KVLND | PEL | FAQ | WED | DLRT | MSGR | IVEM | RKGLRQRL : 374 | | | |
| Ncra-Aat2 : | --PDA | ASIT | TRVASQ | LAIL | LORSE | ISNPP | IYGAK | VASIV | LN | DPA | LFA | EWKEN | DLRT | MSGR | IIDM | RKALRAKL : 411 | | | |
| Mgri-Aat2 : | --AEA | ETTK | RVASQ | LAIL | LORSE | ISNPP | IYGAR | VASIV | LN | DPA | LMS | EWREN | DLRT | MSGR | IITM | RNELRAKL : 386 | | | |
| Bfuc-Aat2 : | --EDA | EKN | RIARIS | SQ | LAIL | LORSE | ISNPP | PAYG | ARIAS | TILN | DESL | FKWEEN | DLRT | MSGR | IITM | RKELRSKL : 345 | | | |
| Sscl-Aat2 : | --PDA | EQT | IGRIASQ | LAIL | LORSE | ISNPP | PAYG | ARIAS | TILN | DEAL | FKWEEN | DLRT | MSGR | IMT | RKELRSKL : 345 | | | | |
| Pnod-Aat2 : | --SDA | ETT | VKRIASQ | LAIL | LORSE | ISNPP | PAYG | ARIAS | TILN | DPK | LFA | EWEN | DLRT | MSGR | IKEM | RTALRSKL : 376 | | | |
| Ccin-Aat2 : | --PDA | ETAN | -RVR | SQ | LSVL | LORSE | ISNPP | SHGARI | VSLN | DP | ELFE | EWKR | DIVT | MSSR | IIDM | RKELYRL : 354 | | | |
| Scer-Aat2 : | --AQN | KT | -IKPA | VT | SQ | LAKT | IRSE | VSNPP | PAYG | AKIV | VAKL | LET | PELT | EQW | HKDM | VTMSS | RITK | MRHALRDHL : 342 | |
| Cgla-Aat2 : | --NAN | LAPI | KS | AIT | SQ | ISSI | IRSE | VSNPP | PAYG | AKIV | SKIL | NTP | ELT | KQW | HEDM | VTMSS | RIKEM | RIALRDHL : 343 | |
| Klac-Aat2 : | --SNV | NVST | ITKAV | SQ | ISKI | TRSE | VSNPP | PAYG | AKIV | VAKI | LNN | AE | LT | EQW | HKDM | VTMSS | ORIT | KMRHSLRDKL : 345 | |
| Agos-Aat2 : | --PAE | SLAH | VKA | AVLSQ | LSH | ITRSE | VSNPP | PAYG | AKIV | TKVL | TTP | ELAA | QW | KDM | VTMSS | SRIAR | MRRVLRDL : 344 | | |
| Calb-Aat2 : | --VES | ND | SLNR | AIKSQ | LNRI | TRSE | VSNPP | PAYG | SKIV | ATIL | N | DP | ELYSQ | WRK | DIVT | MSSR | IGEM | RNTRLSKL : 341 | |
| Dhan-Aat2 : | --AEN | DKSL | NNAI | KSQ | LNKL | TRSE | ISNPP | PAYG | AKIV | VATIL | T | DS | EL | RQW | ED | DLVT | MSSR | INKM | RTLRDL : 344 |

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      *           440           *           460           *           480           *
Cimm-Aat2 : EQK-GTPGTWEHITNOIGMFSFTGLTEQQVGLIREKWHVYMTKNGRISMAGLNTNNIDYFAEAVDSVVRRE : 471
Pchr-Aat2 : EKR-GTPGSWDHITSQIGMFSFTGLSEEQVLTIRSKWHVYMTKNGRISMAGLNTNNIDYFAEAVDSVVRRE : 432
Aory-Aat2 : EAK-GTPGTWNHVITDQIGMFSFTGLSEAQVKLIREKWHIYMTKNGRISMAGLNTNNIDYFAEAVDSVVRRE : 441
Afum-Aat2 : EAK-GTPGNWEHITSQIGMFSFTGLTEEQVKILIREKWHVYMTKNGRISMAGLNTNNIDYFAEAVDSVVRRE : 467
Anid-Aat2 : EEK-KTPGSWNHITDQIGMFSFTGLSEAQVKLIREKWHVYMTKNGRISMAGLNTNNIDYFAEAVDSVVRRE : 443
Ncra-Aat2 : EEL-GTPGPWNHITDQIGMFSFTGLNEKQVAKLREEFHVYMTKNGRISMAGLNTNNIDYFAEAVDSVVRRE : 480
Mgri-Aat2 : EAL-GTPGTWNHITDQIGMFSFTGLTEAQVVKIRSDYHVYMTKNGRISMAGLNTNNIDYFAEAVDSVVRRE : 455
Bfuc-Aat2 : EEM-GTPGKWNHITDQIGMFSFTGLSEKQVMEIRDEAHVYMTKNGRISMAGLNTNNIDYFAEAVDSVVRRE : 414
Sscl-Aat2 : EEM-GTPGKWNHITDQIGMFSFTGLTEKQVLEIRSEAHVYMTKNGRISMAGLNTNNIDYFAEAVDSVVRRE : 414
Pnod-Aat2 : EEL-GTPGTWNHITDQIGMFSFTGLTEQQVVKIRSDYHVYMTKNGRISMAGLNTNNIDYFAEAVDSVVRRE : 445
Ccin-Aat2 : TEVYKTPGNWDHILNQIGMFSFTGLNPEQSKAMVEKAHIYMTGNRISMAGLNTNNIDYFAEAVDSVVRRE : 424
Scer-Aat2 : VK-LGTPGNWDHIVNOCGMFSFTGLTPQMVKRLREETHAVYLVASGRASIAGLNTNNIDYFAEAVDSVVRRE : 411
Cgla-Aat2 : VK-LGTPGTWDHIVECCGMFSFTGLTPEMVKRLRETHAVYLVSSGRASIAGLNTNNIDYFAEAVDSVVRRE : 412
Klac-Aat2 : LE-LQTPGNWDHIVNOCGMFSFTGLTKPMVERLEKEHGVYMTKNGRISMAGLNTNNIDYFAEAVDSVVRRE : 414
Agos-Aat2 : VE-LGTPGNWDHIVQCCGMFSFTGLTKEMVAREKDFAIYMTKNGRISMAGLNTNNIDYFAEAVDSVVRRE : 413
Calb-Aat2 : ES-LGTPGTWNHITDQIGMFSFTGLTPQMVERLEKHHGIYLVSSGRASVAGLNTNNIDYFAEAVDSVVRRE : 410
Dhan-Aat2 : TNQYSTPGNWDHIVSQSGMFSFTGLTPDMVSRLEKNHGIYLVSSGRASVAGLNTNNIDYFAEAVDSVVRRE : 414

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Cimm-Aat2 : TSS----- : 474
Pchr-Aat2 : SAKL----- : 436
Aory-Aat2 : TS----- : 443
Afum-Aat2 : TS----- : 469
Anid-Aat2 : TS----- : 445
Ncra-Aat2 : VQ----- : 482
Mgri-Aat2 : TQ----- : 457
Bfuc-Aat2 : TQQESAKL : 422
Sscl-Aat2 : TQQETANL : 422
Pnod-Aat2 : TQ----- : 447
Ccin-Aat2 : EL----- : 426
Scer-Aat2 : YTIEAKL- : 418
Cgla-Aat2 : YSTSKL-- : 418
Klac-Aat2 : FNESSKL- : 421
Agos-Aat2 : FSTPKL-- : 419
Calb-Aat2 : FGKSKL-- : 416
Dhan-Aat2 : YSKSKL-- : 420

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Legend to Supplementary Fig. S1.

Sequence alignment of fungal microbody-located aspartate transaminases (Aat2).

The following accession numbers were used:

Fungi:

Cimm, *Coccidioides immitis* (EAS29116-corrected); Pchr, *Penicillium chrysogenum* (Pc22g19440); Aory, *Aspergillus oryzae* (BAE65140); Afum, *Aspergillus fumigatus* (EAL93260); Anid, *Aspergillus nidulans* (EAA58023); Ncra, *Neurospora crassa* (EAA33221); Mgri, *Magnaporthe grisea* (EDJ99457); Bfuc, *Botryotinia fuckeliana* (EDN20556); Sscl, *Sclerotinia sclerotiorum* (EDN99237); Pnod, *Phaeosphaeria nodorum* (translation of AAGI01000295, nt 39726-38235); Ccin, *Coprinopsis cinerea* (EAU88611).

Yeast species:

Scer, *Saccharomyces cerevisiae* (NP_013127); Cgla, *Candida glabrata* (CAG58407); Klac, *Kluyveromyces lactis* (CAG98584); Agos, *Ashbya gossypii* (AAS53582); Calb, *Candida albicans* (EAK91905); Dhan, *Debaryomyces hansenii* (CAG87700).

Sequences were aligned using the Clustal_X programme (Thompson et al. 1997). Gaps were introduced to maximize the similarity. Residues that are similar in all 17 proteins are represented by white letters that are shaded black. Similar residues in at least 14 of the proteins are shown as white letters that are shaded dark grey, while those that are similar in at least 11 of the proteins are shown as black letters that are shaded light grey. Putative PTS1 sequences are shaded red; putative PTS2 sequences are in yellow, while the Met residue that immediately follows the putative PTS2 sequences is shown in white on a blue background.

Reference: (for Figs S1, S2 and S3)

1. Thompson JD, Gibson TJ, Plewniak F et al (1997) The ClustalX windows interface: flexible strategies for multiple sequence alignment aided by quality analysis tools. *Nucleic Acids Res* 24:4876-4882